

PIPELINES INTO BIOSTATISTICS

Alumni Poster Abstracts

Gene Expression Networks of Histone Methyltransferases SET1 and SET5 in *S. Cerevisiae*

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Histone methyltransferases Set1 and Set5 play key roles in the modification of chromatin to regulate gene expression. In 2014, Martin *et al.* characterized new functional consequences of losing either one or both Set1 and Set5 in budding yeast. This work revealed that both methyltransferases are important for repressing lowly expressed genes near telomeres and retrotransposons. Our study revisits this raw data and performs alternative methods of RNA-seq analysis for gene expression profiling under a Bioconductor/R pipeline and CLC Genomics workbench protocol. After determining significant differentially expressed genes compared to a wild type (WT) strain, we performed hierarchical clustering and correlation analysis between the *set1Δ*, *set5Δ*, and *set1Δ set5Δ* mutants and microarray data of 16 additional strains lacking well-known chromatin regulators. Clustering based on a Pearson's correlation distance matrix indicates Set5 has an overlapping role with the histone deacetylase Rpd3 and Set1 works in tandem with COMPASS complex components. Preliminary gene ontology (GO) analysis shows significant enrichment for genes involved in sporulation in the *set1Δ* and *set1Δ set5Δ* datasets, suggesting an additional function of these histone methyltransferases. Overall, this method of RNA-seq analysis expands our understanding of Set1 and Set5's function and pathway relationships in the regulation of gene expression.

This work was funded, in part, through an Undergraduate Biology Mathematics (UBM) Award from the National Science Foundation under Grant No. DBI 103140, PIs Drs. Leips and Neerchal.